



NIH133.1CPC1.TXT

SEQUENCE LISTING

<110> Luyten, Frank P.  
Moos, Malcolm J.R.  
Hoang, Bang  
Wang, Shouwen

<120> ISOLATION AND USE OF TISSUE  
GROWTH-INDUCING FRZB PROTEIN

<130> NIH133.1CPC1

<140> US 10/028051

<141> 2001-12-19

<150> US 08/822333

<151> 1997-03-20

<150> US 08/729,452

<151> 1996-10-11

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2374

<212> DNA

<213> Bos taurus

<400> 1

```
aatagatgcc gcgccccag aagtcttaga cgctcggaag gagcagccgg agaggcaggg 60
gcggcgccgg ctggcgctcg gcgcagcttt tgggacccca ttgagggaa ttgatccaag 120
gaagctgtga gattgccggg ggaggagaag ctcccatatc atttgttcca cttccagggc 180
ggggaggagg aaacggcgga gcgggcctct cgcgcttctc cgactgtctg caccctgccc 240
catctgccc agatctaggt ctgcgggagc cgaggcgga tgctgtgct gccggccggg 300
ctactcgccc tgctgctgt ctgcctgctc cgctgctcgg gagcgccggc ggccgctgt 360
gagcccgctt gcattccctt gtgcaagtc ctgcccctga acatgactaa gatgcccaac 420
cacctgcacc acagcacc caaccaacgc atcttgccca tcgagcagtt cgaaggctctg 480
ctgggcaccc actgcagccc ggatctgtct ttcttctct gtgctatgta cgcgcccac 540
tgacccattg acttccagca cgagcccatc aagccctgca agtctgtgtg cgagcgggccc 600
cggcagggct gtgagcccat cctcatcaag taccgccact cgctggccga aagcctggcc 660
tgcgaggagc tgccagtata tgaccgcggc gtgtgcatct ctccggaggc catcgtcact 720
gccgacggag ccgattttcc tatggattcc agtaattgaa actgtagagg agcaagcagt 780
gaacgctgca aatgtaaacc agtcagagct acacagaaga cctatttccg aaacaattac 840
aactatgtca ttcgggctaa agttaagaa ataaagacca agtgtcatga tgtgactgca 900
gtagtggagg tgaaggagat ttaaaaggct tctctggtaa acattccaag ggaactgtg 960
aacctttata ccagctctgg ctgcctgtgt cctccactta acgttaatga ggagtatctc 1020
atcatgggct acgaagatga agagcgctcc agattactgt tggtagaagg ttctattgct 1080
gagaaattga aggatcgact tggtaaaaaa gttaagcggg gggatatgaa gctccgctcat 1140
cttgagctga atacaagtga ttctagccat agtgattcca ctacagatca gaagcctggc 1200
aggaattcta actcccgga agcagcaac taaatcctga aatgcagaaa atcctcagt 1260
gacttcctat taagacttgc attgctggac tagcaaaagg aaattgcact attgcacgtc 1320
atagcttatt ttttagccac aaaaatcagg tggtaactga tattacttct atttttctt 1380
ttgtttctg ctttctctct tccccattc cttttttgt ggtctgagta cagatcctta 1440
aatatattat atgtattcta tttcactaat catgggaaaa ctgttctttg caataataat 1500
aaattaaaca tgtgataacc agggcctctt tgctggagta aatgttaatt tgctgttctg 1560
caccagatt gggaatgcaa tattggatgc aaagagagat ttctggtata cagagaaagc 1620
tagataggct gtaaaagcata ctttgctgat ctaattacag cctcattctt gcatgccttt 1680
tgccattctc ctacgcctta gaaagttcta aatgtttata aaggtaaaaa gacagtttga 1740
aatcaaatgc caacaggcag agcaatcaag caccaggaag catttatgaa gaaatgacac 1800
atgagatgaa ttatttgcaa gattggcagg aagcaaaata aatagcatta ggagctgggg 1860
atagagcatt ttgcctgact gagaagcaca actgaagcta gtagctgttg ggggtttaac 1920
agcagcattt ttcttttgac gatacatttg ttgtctgtg aatataattga tcagcattag 1980
agcagtggtg tgtgaccaga catcagggtg tatcagcata gctctgttta atttgcttcc 2040
ttttagatga acgcatgtgt gtcttttttt tcttctttta aaataaatct cccttgctgc 2100
atttgaccag gaaaagaaag catatatgca tgtgcaccgg gctgttattt ttaagatatg 2160
tagctctata aaacgctata gtcaaaaagt ggtaaaatgt gcaagattct ggggtgtgtg 2220
attaatgtgt gtgtgtccgc atcacctcac actcaagctg aagtgaacga caggcctgtg 2280
cactggcctg cactttatca ttgggatttg tgctgtttaa tgctcagtaa aatatgctta 2340
ataaaaggaa aaaaaaaaaa aaaaaaaaaa aaaa 2374
```

<210> 2

<211> 325

<212> PRT

<213> Bos taurus

<400> 2

NIH133.1CPC1.TXT

Met	Val	Cys	Gly	Ser	Arg	Gly	Gly	Met	Leu	Leu	Pro	Ala	Gly	Leu
1				5				10				15		
Leu	Ala	Leu	Ala	Ala	Leu	Cys	Leu	Leu	Arg	Val	Pro	Gly	Ala	Arg
			20					25				30		Ala
Ala	Ala	Cys	Glu	Pro	Val	Arg	Ile	Pro	Leu	Cys	Lys	Ser	Leu	Pro
		35				40					45			Trp
Asn	Met	Thr	Lys	Met	Pro	Asn	His	Leu	His	His	Ser	Thr	Gln	Ala
	50					55					60			Asn
Ala	Ile	Leu	Ala	Ile	Glu	Gln	Phe	Glu	Gly	Leu	Leu	Gly	Thr	His
65					70					75				Cys
Ser	Pro	Asp	Leu	Leu	Phe	Phe	Leu	Cys	Ala	Met	Tyr	Ala	Pro	Ile
			85					90					95	Cys
Thr	Ile	Asp	Phe	Gln	His	Glu	Pro	Ile	Lys	Pro	Cys	Lys	Ser	Val
			100					105					110	Cys
Glu	Arg	Ala	Arg	Gln	Gly	Cys	Glu	Pro	Ile	Leu	Ile	Lys	Tyr	Arg
		115					120					125		His
Ser	Trp	Pro	Glu	Ser	Leu	Ala	Cys	Glu	Glu	Leu	Pro	Val	Tyr	Asp
		130				135					140			Arg
Gly	Val	Cys	Ile	Ser	Pro	Glu	Ala	Ile	Val	Thr	Ala	Asp	Gly	Ala
145					150					155				Asp
Phe	Pro	Met	Asp	Ser	Ser	Asn	Gly	Asn	Cys	Arg	Gly	Ala	Ser	Ser
			165					170					175	Glu
Arg	Cys	Lys	Cys	Lys	Pro	Val	Arg	Ala	Thr	Gln	Lys	Thr	Tyr	Phe
			180					185					190	Arg
Asn	Asn	Tyr	Asn	Tyr	Val	Ile	Arg	Ala	Lys	Val	Lys	Glu	Ile	Lys
		195					200					205		Thr
Lys	Cys	His	Asp	Val	Thr	Ala	Val	Val	Glu	Val	Lys	Glu	Ile	Leu
		210				215					220			Lys
Ala	Ser	Leu	Val	Asn	Ile	Pro	Arg	Glu	Thr	Val	Asn	Leu	Tyr	Thr
225					230					235				Ser
Ser	Gly	Cys	Leu	Cys	Pro	Pro	Leu	Asn	Val	Asn	Glu	Glu	Tyr	Leu
			245					250						Ile
Met	Gly	Tyr	Glu	Asp	Glu	Glu	Arg	Ser	Arg	Leu	Leu	Leu	Val	Glu
			260					265					270	Gly
Ser	Ile	Ala	Glu	Lys	Trp	Lys	Asp	Arg	Leu	Gly	Lys	Lys	Val	Lys
		275					280					285		Arg
Trp	Asp	Met	Lys	Leu	Arg	His	Leu	Gly	Leu	Asn	Thr	Ser	Asp	Ser
		290				295					300			Ser
His	Ser	Asp	Ser	Thr	Gln	Ser	Gln	Lys	Pro	Gly	Arg	Asn	Ser	Asn
305					310					315				Ser
Arg	Gln	Ala	Arg	Asn										
				325										

<210> 3  
 <211> 1484  
 <212> DNA  
 <213> Homo sapiens

<400> 3

cggggccttg	gcggsagggg	cggtggctgg	agctcggtaa	agctcgtggg	acccatttgg	60
gggaatttga	tccaagggaag	cggtgattgc	cgggggagga	gaagctccca	gatccttgtg	120
tccacttgca	gcgggggagg	cggagacgcg	gagcgggcct	tttgcgctcc	actgcgcggc	180
tgcaccctgc	cccatcctgc	cgggatcatg	gtctgcggca	gcccgggagg	gatgctgctg	240
ctgcgggccc	ggctgcttgc	cctggctgct	ctctgcctgc	tccgggtgcc	cggggctcgg	300
gctgcagcct	gtgagcccgt	ccgcattccc	ctgtgcaagt	ccctgccctg	gaacatgact	360
aagatgccca	accacctgca	ccacagcact	caggccaacg	ccatcctggc	catcgagcag	420
ttcgaaggtc	tgctgggcac	ccactgcagc	cccgatctgc	tcttcttctt	ctgtgccatg	480
tacgcgcccc	tctgcaccat	tgacttccag	cacgagcccc	tcaagccctg	taagtctgtg	540
tgcgagcggg	cccggcaggg	ctgtgagccc	atactcatca	agtaccgcca	ctcgtggccg	600
gagaacctgg	cctgcgagga	gctgccagtg	tacgacaggg	gcgtgtgcat	ctctcccag	660
gccatcggtt	ctgcggacgg	agctgatttt	cctatggatt	ctagttaacg	aaactgtaga	720
ggggcaagca	gtgaacgctg	taaatgtaag	cctattagag	ctacacagaa	gacctatttc	780
cggaacaatt	acaactatgt	cattcgggct	aaagttaaag	agataaagac	taagtgccat	840
gatgtgactg	cagtagtgga	ggtgaaggag	attctaaagt	cctctctggt	aaacattcca	900
cgggacactg	tcaacctcta	taccagctct	ggctgcctct	gccctccact	taatgttaat	960
gaggaatatg	ctatcatggg	ctatgaagat	gaggaacggt	ccagattact	cttgggtggaa	1020
ggctctatag	ctgagaagtg	gaaggatcga	ctcggtaaaa	aagttaagcg	ctgggatatg	1080
aagcttcgtc	atcttgactg	cagtaaaagt	gattctagca	atagtgaatt	cactcagagt	1140
cagaagctctg	gcagggaactc	gaacccccgg	caagcacgca	actaaatccc	gaaatacaaa	1200
aagtaacaca	gtggacttcc	tattaagact	tacttgcatt	gctggactag	caaggaaaaa	1260
ttgcactatt	gcacatcata	ttctattggt	tactataaaa	atcatgtgat	aactgattat	1320
tacttctgtt	ttctttttgg	tttctgttct	tctcttctct	caaccccttt	gtaatgggtt	1380
gggggcagac	ttctaagtat	attgtgagtt	ttctatttca	ctaactcatga	gaaaaactgt	1440
tcttttgcaa	taataataaa	ttaaactatg	tgtaaaaaaa	aaaa		1484

<210> 4  
 <211> 325  
 <212> PRT

<213> Homo sapiens

<400> 4

```

Met Val Cys Gly Ser Pro Gly Gly Met Leu Leu Leu Arg Ala Gly Leu
 1      5      10      15
Leu Ala Leu Ala Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala
 20      25      30
Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
 35      40      45
Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
 50      55      60
Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
 65      70      75
Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
 85      90      95
Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
100      105      110
Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
115      120      125
Ser Trp Pro Glu Asn Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg
130      135      140
Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
145      150      155
Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu
160      165      170
Arg Cys Lys Cys Lys Pro Ile Arg Ala Thr Gln Lys Thr Tyr Phe Arg
175      180      185
Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr
190      195      200
Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
205      210      215
Ser Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Ser
220      225      230
Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Ile Ile
235      240      245
Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
250      255      260
Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
265      270      275
Trp Asp Met Lys Leu Arg His Leu Gly Leu Ser Lys Ser Asp Ser Ser
280      285      290
Asn Ser Asp Ser Thr Gln Ser Gln Lys Ser Gly Arg Asn Ser Asn Pro
300      305      310
Arg Gln Ala Arg Asn
315      320      325

```

<210> 5

<211> 111

<212> PRT

<213> Rattus norvegicus

<400> 5

```

Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp Ile Ala Tyr Asn Gln
 1      5      10      15
Thr Ile Met Pro Asn Leu Leu Gly His Thr Asn Gln Glu Asp Ala Gly
 20      25      30
Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys Val Gln Cys Ser Ala
 35      40      45
Glu Leu Lys Phe Phe Leu Cys Ser Met Tyr Ala Pro Val Cys Thr Val
 50      55      60
Leu Glu Gln Ala Leu Pro Pro Cys Arg Ser Leu Cys Glu Arg Ala Gln
 65      70      75
Gly Cys Glu Ala Leu Met Asn Lys Phe Gly Phe Gln Trp Pro Asp Thr
 80      85      90
Leu Lys Cys Glu Lys Phe Pro Val His Gly Arg Gly Glu Leu Cys
 95      100      105      110

```

<210> 6

<211> 111

<212> PRT

<213> Drosophila melanogaster

<400> 6

```

Cys Glu Pro Ile Thr Ile Ser Ile Cys Lys Asn Ile Pro Tyr Asn Met
 1      5      10      15
Thr Ile Met Pro Asn Leu Ile Gly His Thr Lys Gln Glu Glu Ala Gly
 20      25      30

```

NIH133.1CPC1.TXT

Leu Glu Val His Gln Phe Ala Pro Leu Val Lys Ile Gly Cys Ser Asp  
 35 40 45  
 Asp Leu Gln Leu Phe Leu Cys Ser Leu Tyr Val Pro Val Cys Thr Ile  
 50 55 60  
 Leu Glu Arg Pro Ile Pro Cys Arg Ser Leu Cys Glu Ser Ala Arg  
 65 70 75 80  
 Val Cys Glu Lys Leu Met Lys Thr Tyr Asn Phe Asn Trp Pro Glu Asn  
 85 90 95  
 Leu Glu Cys Ser Lys Phe Pro Val His Gly Gly Glu Asp Leu Cys  
 100 105 110

<210> 7  
 <211> 319  
 <212> PRT  
 <213> Xenopus laevis

<400> 7  
 Met Ser Pro Thr Arg Lys Leu Asp Ser Phe Leu Leu Leu Val Ile Pro  
 1 5 10 15  
 Gly Leu Val Leu Leu Leu Leu Pro Asn Ala Tyr Cys Ala Ser Cys Glu  
 20 25 30  
 Pro Val Arg Ile Pro Met Cys Lys Ser Met Pro Trp Asn Met Thr Lys  
 35 40 45  
 Met Pro Asn His Leu His His Ser Thr Gln Ala Asn Ala Ile Leu Ala  
 50 55 60  
 Ile Glu Gln Phe Glu Gly Leu Leu Thr Thr Glu Cys Ser Gln Asp Leu  
 65 70 75 80  
 Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys Thr Ile Asp Phe  
 85 90 95  
 Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys Glu Arg Ala Arg  
 100 105 110  
 Ala Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His Thr Trp Pro Glu  
 115 120 125  
 Ser Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg Gly Val Cys Ile  
 130 135 140  
 Ser Pro Glu Ala Ile Val Thr Val Glu Gln Gly Thr Asp Ser Met Pro  
 145 150 155 160  
 Asp Phe Pro Met Asp Ser Asn Asn Gly Asn Cys Gly Ser Thr Ala Gly  
 165 170 175  
 Glu His Cys Lys Cys Lys Pro Met Lys Ala Ser Gln Lys Thr Tyr Leu  
 180 185 190  
 Lys Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys  
 195 200 205  
 Val Lys Cys His Asp Ala Thr Ala Ile Val Glu Val Lys Glu Ile Leu  
 210 215 220  
 Lys Ser Ser Leu Val Asn Ile Pro Lys Asp Thr Val Thr Leu Tyr Thr  
 225 230 235 240  
 Asn Ser Gly Cys Leu Cys Pro Gln Leu Val Ala Asn Glu Glu Tyr Ile  
 245 250 255  
 Ile Met Gly Tyr Glu Asp Lys Glu Arg Thr Arg Leu Leu Leu Val Glu  
 260 265 270  
 Gly Ser Leu Ala Glu Lys Trp Arg Asp Arg Leu Ala Lys Lys Val Lys  
 275 280 285  
 Arg Trp Asp Gln Lys Leu Arg Pro Arg Lys Ser Lys Asp Pro Val  
 290 295 300  
 Ala Pro Ile Pro Asn Lys Asn Ser Asn Ser Arg Gln Ala Arg Ser  
 305 310 315

<210> 8  
 <211> 319  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus sequence

<400> 8  
 Met Val Cys Gly Ser Gly Gly Met Leu Leu Leu Ala Gly Leu Leu Ala  
 1 5 10 15  
 Leu Ala Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala Ala Ala  
 20 25 30  
 Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp Asn Met  
 35 40 45  
 Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn Ala Ile  
 50 55 60  
 Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys Ser Pro  
 65 70 75 80

NIH133.1CPC1.TXT

Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys Thr Ile  
 85 90 95  
 Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys Glu Arg  
 100 105 110  
 Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His Ser Trp  
 115 120 125  
 Pro Glu Ser Leu Ala Cys Glu Leu Pro Val Tyr Asp Arg Gly Val  
 130 135 140  
 Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp Phe Pro  
 145 150 155 160  
 Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu Arg Cys  
 165 170 175  
 Lys Cys Lys Pro Arg Ala Thr Gln Lys Thr Tyr Phe Arg Asn Asn Tyr  
 180 185 190  
 Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr Lys Cys His  
 195 200 205  
 Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys Ser Ser Leu  
 210 215 220  
 Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Ser Ser Gly Cys  
 225 230 235 240  
 Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Ile Ile Met Gly Tyr  
 245 250 255  
 Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly Ser Ile Ala  
 260 265 270  
 Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg Trp Asp Met  
 275 280 285  
 Lys Leu Arg His Leu Gly Leu Ser Asp Ser Ser Ser Asp Ser Thr Gln  
 290 295 300  
 Ser Gln Lys Pro Gly Arg Asn Ser Asn Ser Arg Gln Ala Arg Asn  
 305 310 315

<210> 9  
 <211> 30  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic peptide

<400> 9  
 Glu Thr Val Asn Leu Tyr Thr Ser Ala Gly Cys Leu Cys Pro Pro Leu  
 1 5 10 15  
 Asn Val Asn Glu Glu Tyr Leu Ile Met Gly Tyr Glu Phe Pro  
 20 25 30

<210> 10  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide primer

<221> misc\_feature  
 <222> (1)...(21)  
 <223> n = A,T,C or G

<400> 10  
 garachgtsa aycbtayac n

21

<210> 11  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide primer

<221> misc\_feature  
 <222> (1)...(18)  
 <223> n = A,T,C or G

<400> 11  
 raaytcrtan cccatnat

18

<210> 12  
 <211> 19

<212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> tryptic fragment  
 <221> VARIANT  
 <222> (1)...(19)  
 <223> Xaa = Asp or His  
 <400> 12  
 Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Xaa Gly Ala Asp  
 1 5 10 15  
 Phe Pro Met

<210> 13  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> tryptic fragment  
 <400> 13  
 Gln Gly Cys Glu Pro Ile Leu Ile Lys  
 1 5

<210> 14  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> tryptic fragment  
 <400> 14  
 Gln Gly Cys Glu Pro Ile Leu Ile Cys Ala Trp Pro Pro Leu Tyr  
 1 5 10 15

<210> 15  
 <211> 28  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> tryptic fragment  
 <400> 15  
 Glu Thr Val Asn Leu Tyr Thr Ser Ala Gly Cys Leu Cys Pro Pro Leu  
 1 5 10 15  
 Asn Val Asn Glu Glu Tyr Leu Ile Met Gly Tyr Glu  
 20 25

<210> 16  
 <211> 28  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> synthetic peptide  
 <400> 16  
 Glu Thr Val Asn Leu Tyr Thr Ser Ser Gly Cys Leu Cys Pro Pro Leu  
 1 5 10 15  
 Asn Val Asn Glu Glu Tyr Leu Ile Met Gly Tyr Glu  
 20 25

<210> 17  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>

```

<223> oligonucleotide primer
<400> 17
gctctggctg cctgtgtcct ccacttaacg          30
<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer
<400> 18
cctccactta acgttaatga ggagtatctc          30
<210> 19
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer
<400> 19
tggaacatga ctaagatgcc c                    21
<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer
<400> 20
catatactgg cagctcctcg                      20
<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer
<400> 21
gtcttttggg aagccttcat gg                  22
<210> 22
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer
<400> 22
gcatcgtggc atttcacttt ca                  22
<210> 23
<211> 1291
<212> DNA
<213> Xenopus laevis

<400> 23
tttactgtgc cagtcctccc tgtaaccagc gacctgtatt cccccaagta agcctacaca 60
tacagggttg gcagaataac aatgtctcca acaaggaaat tggactcatt cctgtacttg 120
gtcatacctg gactgggtgct tctcttatta cccaatgctt actgtgcttc gtgtgagcct 180
gtgcggattc ccatgtgcaa atctatgcca tggaacatga ccaagatgcc caaccatctc 240
caccacagca ctcaagccaa tgctatcctg gcaattgaac agtttgaagg ttgtctgacc 300
actgaatgta gccaggacct tttgttcttt ctgtgtgcca tgtatgcccc catttgacc 360
atcgatttcc agcatgaacc aattaagcct tgcaagtcct tgtgcgaaa ggccagggcc 420
ggctgtgagc ccattctcat aaagtaccgg cacacttggc cagagagcct ggcatgtgaa 480
gagctgcccg tatatgacag aggagtctgc atctccccag aggctatcgt cacagtggaa 540
caagggaacag attcaatgcc agacttcccc atggattcaa acaatggaaa ttgcggaagc 600
acggcaggtg agcactgtaa atgcaagccc atgaaaggctt cccaaaagac gtatctcaag 660
aataattaca attatgtaat cagagcaaaa gtgaaagagg tgaaagtgaa atgccacgac 720
gcaacagcaa ttgtggaagt aaaggagatt ctcaagtctt ccctagttaa cattcctaaa 780

```

NIH133.1CPC1.TXT

```

gacacagtga cactgtacac caactcaggc tgcttgtgcc cccagcttgt tgccaatgag 840
gaatacataa ttatgggcta tgaagacaaa gagcgtacca ggcttctact agtgggaagga 900
tccttggccg aaaaatggag agatcgtctt gctaagaaaag tcaagcgctg ggatcaaaaag 960
cttcgacgtc ccaggaaaag caaagacccc gtggctccaa ttccaacaa aaacagcaat 1020
tccagacaag cgcgtagtta gactaacgga aagggtgatg gaaactctat ggactttgaa 1080
actaagattt gcattgttgg aagagcaaaa aagaaattgc actacagcac gttatattct 1140
attgtttact acaagaagct ggtttagttg attgtagttc tcctttcctt ctttttttta 1200
taactatatt gcacgtgttc caggcagttt atcaacttcc agtgacagag cagtgactga 1260
atgtagctaa gagcctatca tctgatcact a                                     1291

```